

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
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Application Serial Number: 10/767,809A
Source: 1FW/6
Date Processed by STIC: 3/7/07

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IFW16

RAW SEQUENCE LISTING

DATE: 03/07/2007

PATENT APPLICATION: US/10/767,809A

TIME: 09:24:03

Input Set : A:\PC25496A US Sequence Listing.txt

Output Set: N:\CRF4\03072007\J767809A.raw

```

3 <110> APPLICANT: Pfizer Inc.
4     Dominowski, Paul J.
5     Frantz, Joseph C.
6     Krebs, Richard L.
7     Shields, Shelly L.
8     Sorensen, Robert G.
10 <120> TITLE OF INVENTION: Canine Vaccines Against Bordetella Bronchiseptica
12 <130> FILE REFERENCE: PC25496A
14 <140> CURRENT APPLICATION NUMBER: 10/767809A
15 <141> CURRENT FILING DATE: 2004-01-29
17 <150> PRIOR APPLICATION NUMBER: 60/443,418
18 <151> PRIOR FILING DATE: 2003-01-29
20 <160> NUMBER OF SEQ ID NOS: 3
22 <170> SOFTWARE: PatentIn version 3.3
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 602
26 <212> TYPE: PRT
27 <213> ORGANISM: Bordetella bronchiseptica
29 <400> SEQUENCE: 1
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35 Ile His Ile Lys Gln Ser Asp Gly Ala Gly Val Arg Thr Ala Thr Gly
36             20             25             30
39 Thr Thr Ile Lys Val Ser Gly Arg Gln Ala Gln Gly Val Leu Leu Glu
40             35             40             45
43 Asn Pro Ala Ala Glu Leu Arg Phe Gln Asn Gly Ser Val Thr Ser Ser
44             50             55             60
47 Gly Gln Leu Phe Asp Glu Gly Val Arg Arg Phe Leu Gly Thr Val Thr
48 65             70             75             80
51 Val Lys Ala Gly Lys Leu Val Ala Asp His Ala Thr Leu Ala Asn Val
52             85             90             95
55 Ser Asp Thr Arg Asp Asp Asp Gly Ile Ala Leu Tyr Val Ala Gly Glu
56             100            105            110
59 Gln Ala Gln Ala Ser Ile Ala Asp Ser Thr Leu Gln Gly Ala Gly Gly
60             115            120            125
63 Val Arg Val Glu Arg Gly Ala Asn Val Thr Val Gln Arg Ser Thr Ile
64             130            135            140
67 Val Asp Gly Gly Leu His Ile Gly Thr Leu Gln Pro Leu Gln Pro Glu
68 145            150            155            160
71 Asp Leu Pro Pro Ser Arg Val Val Leu Gly Asp Thr Ser Val Thr Ala
72             165            170            175
75 Val Pro Ala Ser Gly Ala Pro Ala Ala Val Ser Val Phe Gly Ala Asn
76             180            185            190

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79 Glu Leu Thr Val Asp Gly Gly His Ile Thr Gly Gly Arg Ala Ala Gly
80      195      200      205
83 Val Ala Ala Met Asp Gly Ala Ile Val His Leu Gln Arg Ala Thr Ile
84      210      215      220
87 Arg Arg Gly Asp Ala Pro Ala Gly Gly Ala Val Pro Gly Gly Ala Val
88 225      230      235      240
91 Pro Gly Gly Phe Gly Pro Leu Leu Asp Gly Trp Tyr Gly Val Asp Val
92      245      250      255
95 Ser Asp Ser Thr Val Asp Leu Ala Gln Ser Ile Val Glu Ala Pro Gln
96      260      265      270
99 Leu Gly Ala Ala Ile Arg Ala Gly Arg Gly Ala Arg Val Thr Val Ser
100     275     280     285
103 Gly Gly Ser Leu Ser Ala Pro His Gly Asn Val Ile Glu Thr Gly Gly
104     290     295     300
107 Gly Ala Arg Arg Phe Pro Pro Ala Ser Pro Leu Ser Ile Thr Leu
108 305     310     315     320
111 Arg Ala Gly Ala Arg Ala Gln Gly Arg Ala Leu Leu Tyr Arg Val Leu
112     325     330     335
115 Pro Glu Pro Val Lys Leu Thr Leu Ala Gly Gly Ala Gln Gly Gln Gly
116     340     345     350
119 Asp Ile Val Ala Thr Glu Leu Pro Pro Ile Pro Gly Ala Ser Ser Gly
120     355     360     365
123 Pro Leu Asp Val Ala Leu Ala Ser Gln Ala Arg Trp Thr Gly Ala Thr
124     370     375     380
127 Arg Ala Val Asp Ser Leu Ser Ile Asp Asn Ala Thr Trp Val Met Thr
128 385     390     395     400
131 Asp Asn Ser Asn Val Gly Ala Leu Arg Leu Ala Ser Asp Gly Ser Val
132     405     410     415
135 Asp Phe Gln Gln Pro Ala Glu Ala Gly Arg Phe Lys Val Leu Met Val
136     420     425     430
139 Asp Thr Leu Ala Gly Ser Gly Leu Phe Arg Met Asn Val Phe Ala Asp
140     435     440     445
143 Leu Gly Leu Ser Asp Lys Leu Val Val Met Arg Asp Ala Ser Gly Gln
144     450     455     460
147 His Arg Leu Trp Val Arg Asn Ser Gly Ser Glu Pro Ala Ser Ala Asn
148 465     470     475     480
151 Thr Met Leu Leu Val Gln Thr Pro Arg Gly Ser Ala Ala Thr Phe Thr
152     485     490     495
155 Leu Ala Asn Lys Asp Gly Lys Val Asp Ile Gly Thr Tyr Arg Tyr Arg
156     500     505     510
159 Leu Ala Ala Asn Gly Asn Gly Gln Trp Ser Leu Val Gly Ala Lys Ala
160     515     520     525
163 Pro Pro Ala Pro Lys Pro Ala Pro Gln Pro Gly Pro Gln Pro Gly Pro
164     530     535     540
167 Gln Pro Gly Pro Gln Pro Pro Gln Pro Pro Gln Pro Pro Gln Pro Pro
168 545     550     555     560
171 Gln Arg Gln Pro Glu Ala Pro Ala Pro Gln Pro Pro Ala Gly Arg Glu
172     565     570     575
175 Leu Ser Ala Ala Ala Asn Ala Ala Val Asn Thr Gly Gly Val Gly Leu

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179 Ala Ser Thr Leu Trp Tyr Ala Glu Ser Asn
180          595          600
183 <210> SEQ ID NO: 2
184 <211> LENGTH: 1806
185 <212> TYPE: DNA
186 <213> ORGANISM: Bordetella bronchiseptica
188 <400> SEQUENCE: 2
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191 caaagcgatg gcgcccgcgt acggaccgcc accggaacga ccatcaagggt aagcgggtcgt      120
193 caggcccagg gcgtcctgct ggaaaatccc gcggccgagc tgcggttcca gaacggcagc      180
195 gtcacgtctt cgggacagct gttcgacgaa ggcgtccggc gctttctggg caccgtcacc      240
197 gtcaaggccg gcaagctggt cgcgatcac gccacgtgg ccaacgtcag cgacaccggg      300
199 gacgacgacg gcatcgcgct ctatgtggcc ggcgagcagg cccaggccag catcgccgac      360
201 agcaccctgc agggcgcggg cggcgtgagg gtcgagcgcg gcgccaatgt cacgggtccaa      420
203 cgcagcacca tcgttgacgg gggcttgcat atcggcacc cgcagccgct gcagccggaa      480
205 gaccttcgcg ccagccgggt ggtgctgggc gacaccagcg tgaccgccgt gcccgccagc      540
207 ggcgcgcccc cggcgggtgtc tgtattcggg gccaatgagc ttacggttga tggcgggcac      600
209 atcacggggg ggcgggcagc ggggggtggcg gccatggacg gggcgatcgt gcatctgcag      660
211 cgcgcgacga tacggcgggg ggacgcgcct gccggcggtg cggttccagg cgggtgcggtt      720
213 cccggcggtc tcggccccct ccttgacggc tggtatggcg tggatgtatc ggactccacc      780
215 gtggacctcg ctacgtcgat cgtcgaggcg ccgcagctgg gcgcccgat ccgggcgggc      840
217 cgcggcgcca gggtgacggt gtcgggcggc agcttgctcg caccgcacgg caatgtcatc      900
219 gagaccggcg gcggtgcgcg tcgcttcccg cctccggcct cggccctgtc gatcaccttg      960
221 cgggcggggc cacgggcgca ggggagggcg ctgctgtacc gggctctgcc ggagcccgtg      1020
223 aagctgacgc tggcgggcgg cggccagggg cagggcgaca tcgtcgcgac ggagctgcct      1080
225 cccattccag gcgcgtcgag cgggcccgtc gacgtggcgc tggccagcca ggcccgatgg      1140
227 acgggcgcta cccgcgcggt cgactcgctg tccatcgaca accccacctg ggtcatgacg      1200
229 gacaactcga acgtcggcgc gctgcggctg gccagcgacg gcagcgtcga tttccagcag      1260
231 ccggccgaag ctgggcgggt caaggtcctg atggtcgata cgctggcggg ttcggggctg      1320
233 ttccgcatga atgtcttcgc ggacctgggg ctgagcgaca agctggtcgt catgcgggac      1380
235 gccagcggcc agcacaggct gtgggtccgc aacagcggca gcgagccggc cagcgccaac      1440
237 accatgctgc tgggtgcagac gccacgaggc agcgcggcga cctttaccct tgccaacaag      1500
239 gacggcaagg tcgatatcgg tacctaccgc tatcgattgg ccgccaacgg caatgggcag      1560
241 tggagcctgg tgggcgcgaa ggcgccggcg gcgcccgaag ccgcgccgca gcccggtccc      1620
243 cagcccggtc cccagcccgg tccccagccg ccgcagccgc cgcagccgcc gcagccgcca      1680
245 cagaggcgag cggaagcgcc ggcgcgcgaa ccgccggcgg gcagggagtt gtccgcccgc      1740
247 gccaacgcgg cgggtcaacac ggggtggggtg ggcctggcca gcacgctctg gtacgccgaa      1806
249 agcaat
252 <210> SEQ ID NO: 3
253 <211> LENGTH: 599
254 <212> TYPE: PRT
255 <213> ORGANISM: Bordetella bronchiseptica
257 <400> SEQUENCE: 3
259 Asp Trp Asn Asn Gln Ser Ile Ile Lys Ala Gly Glu Arg Gln His Gly
260 1          5          10          15
263 Ile His Ile Lys Gln Ser Asp Gly Ala Gly Val Arg Thr Ala Thr Gly
264          20          25          30
267 Thr Thr Ile Lys Val Ser Gly Arg Gln Ala Gln Gly Val Leu Leu Glu

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268	35	40	45
271 Asn Pro Ala Ala Glu Leu Arg Phe Gln Asn Gly Ser Val Thr Ser Ser			
272 50 55 60			
275 Gly Gln Leu Phe Asp Glu Gly Val Arg Arg Phe Leu Gly Thr Val Thr			
276 65 70 75 80			
279 Val Lys Ala Gly Lys Leu Val Ala Asp His Ala Thr Leu Ala Asn Val			
280 85 90 95			
283 Ser Asp Thr Arg Asp Asp Asp Gly Ile Ala Leu Tyr Val Ala Gly Glu			
284 100 105 110			
287 Gln Ala Gln Ala Ser Ile Ala Asp Ser Thr Leu Gln Gly Ala Gly Gly			
288 115 120 125			
291 Val Arg Val Glu Arg Gly Ala Asn Val Thr Val Gln Arg Ser Thr Ile			
292 130 135 140			
295 Val Asp Gly Gly Leu His Ile Gly Thr Leu Gln Pro Leu Gln Pro Glu			
296 145 150 155 160			
299 Asp Leu Pro Pro Ser Arg Val Val Leu Gly Asp Thr Ser Val Thr Ala			
300 165 170 175			
303 Val Pro Ala Ser Gly Ala Pro Ala Ala Val Ser Val Phe Gly Ala Asn			
304 180 185 190			
307 Glu Leu Thr Val Asp Gly Gly His Ile Thr Gly Gly Arg Ala Ala Gly			
308 195 200 205			
311 Val Ala Ala Met Asp Gly Ala Ile Val His Leu Gln Arg Ala Thr Ile			
312 210 215 220			
315 Arg Arg Gly Asp Ala Pro Ala Gly Gly Ala Val Pro Gly Gly Ala Val			
316 225 230 235 240			
319 Pro Gly Gly Phe Gly Pro Leu Leu Asp Gly Trp Tyr Gly Val Asp Val			
320 245 250 255			
323 Ser Asp Ser Thr Val Asp Leu Ala Gln Ser Ile Val Glu Ala Pro Gln			
324 260 265 270			
327 Leu Gly Ala Ala Ile Arg Ala Gly Arg Gly Ala Arg Val Thr Val Ser			
328 275 280 285			
331 Gly Gly Ser Leu Ser Ala Pro His Gly Asn Val Ile Glu Thr Gly Gly			
332 290 295 300			
335 Gly Ala Arg Arg Phe Pro Pro Pro Ala Ser Pro Leu Ser Ile Thr Leu			
336 305 310 315 320			
339 Gln Ala Gly Ala Arg Ala Gln Gly Arg Ala Leu Leu Tyr Arg Val Leu			
340 325 330 335			
343 Pro Glu Pro Val Lys Leu Thr Leu Ala Gly Gly Ala Gln Gly Gln Gly			
344 340 345 350			
347 Asp Ile Val Ala Thr Glu Leu Pro Pro Ile Pro Gly Ala Ser Ser Gly			
348 355 360 365			
351 Pro Leu Asp Val Ala Leu Ala Ser Gln Ala Arg Trp Thr Gly Ala Thr			
352 370 375 380			
355 Arg Ala Val Asp Ser Leu Ser Ile Asp Asn Ala Thr Trp Val Met Thr			
356 385 390 395 400			
359 Asp Asn Ser Asn Val Gly Ala Leu Arg Leu Ala Ser Asp Gly Ser Val			
360 405 410 415			
363 Asp Phe Gln Gln Pro Ala Glu Ala Gly Arg Phe Lys Cys Leu Met Val			
364 420 425 430			

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367 Asp Thr Leu Ala Gly Ser Gly Leu Phe Arg Met Asn Val Ala Phe Ala
368           435                      440                      445
371 Asp Leu Gly Leu Ser Asp Lys Leu Val Val Met Arg Asp Ala Ser Gly
372           450                      455                      460
375 Gln His Arg Leu Leu Val Arg Asn Ser Gly Ser Glu Pro Ala Ser Gly
376 465           470                      475                      480
379 Asn Thr Met Leu Leu Val Gln Thr Pro Arg Gly Ser Ala Ala Thr Phe
380           485                      490                      495
383 Thr Leu Ala Asn Lys Asp Gly Lys Val Asp Ile Gly Thr Tyr Arg Tyr
384           500                      505                      510
387 Arg Leu Ala Ala Asn Gly Asn Gly Gln Trp Ser Leu Val Gly Ala Lys
388           515                      520                      525
391 Ala Pro Pro Ala Pro Lys Pro Ala Pro Gln Pro Gly Pro Gln Pro Gly
392           530                      535                      540
395 Pro Gln Pro Pro Gln Pro Pro Gln Pro Pro Gln Pro Pro Gln Arg Gln
396 545           550                      555                      560
399 Pro Glu Ala Pro Ala Pro Gln Pro Pro Ala Gly Arg Glu Leu Ser Ala
400           565                      570                      575
403 Ala Ala Asn Ala Ala Val Asn Thr Gly Gly Val Gly Leu Ala Ser Thr
404           580                      585                      590
407 Leu Trp Tyr Ala Glu Ser Asn
408           595

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VERIFICATION SUMMARY

DATE: 03/07/2007

PATENT APPLICATION: US/10/767,809A

TIME: 09:24:04

Input Set : A:\PC25496A US Sequence Listing.txt

Output Set: N:\CRF4\03072007\J767809A.raw